

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: de la Monte, Suzanne
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 - (B) STREET: 1100 New York Ave., Suite 600
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Esmond, Robert W.
 - (B) REGISTRATION NUMBER: 32,893
 - (C) REFERENCE/DOCKET NUMBER: 0609.4370000
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..1139
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

T T T T T T T T T T G A G A T G G A G T T T C G C T C T T G T T G C C C A G G C T G G A G T G C
Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
   1          5          10          15

Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
   20         25          30

Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
   35         40          45

Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
   50         55          60

Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
   65         70          75          80

Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu

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AAT	GGC	GCA	ATC	TCA	GCT	CAC	CGC	AAC	CTC	CGC	CTC	CCG	GGT	TCA	AGC		98
Asn	Gly	Ala	Ile	Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser		
15								20					25				
GAT	TCT	CCT	GCC	TCA	GCC	TCC	CCA	GTA	GCT	GGG	ATT	ACA	GGC	ATG	TGC		146
Asp	Ser	Pro	Ala	Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys		
30						35				40							
ACC	CAC	GCT	CGG	CTA	ATT	TTG	TAT	TTT	TTT	TTA	GTA	GAG	ATG	GAG	TTT		194
Thr	His	Ala	Arg	Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe		
45						50				55			60				
CTC	CAT	GTT	GGT	CAG	GCT	GGT	CTC	GAA	CTC	CCG	ACC	TCA	GAT	GAT	CCC		242
Leu	His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro		
							65		70				75				
TCC	GTC	TCG	GCC	TCC	CAA	AGT	GCT	AGA	TAC	AGG	ACT	GGC	CAC	CAT	GCC		290
Ser	Val	Ser	Ala	Ser	Gln	Ser	Ala	Arg	Tyr	Arg	Thr	Gly	His	His	Ala		
							80		85			90					
CGG	CTC	TGC	CTG	GCT	AAT	TTT	TGT	GGT	AGA	AAC	AGG	GTT	TCA	CTG	ATG		338
Arg	Leu	Cys	Leu	Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met		
							95		100			105					
TGC	CCA	AGC	TGG	TCT	CCT	GAG	CTC	AAG	CAG	TCC	ACC	TGC	CTC	AGC	CTC		386
Cys	Pro	Ser	Trp	Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu		
							110		115			120					
CCA	AAG	TGC	TGG	GAT	TAC	AGG	CGT	GCA	GCC	GTG	CCT	GGC	CTT	TTT	ATT		434
Pro	Lys	Cys	Trp	Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile		
							125		130			135		140			
TTA	TTT	TTT	TTA	AGA	CAC	AGG	TGT	CCC	ACT	CTT	ACC	CAG	GAT	GAA	GTG		482
Leu	Phe	Phe	Leu	Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val		
							145		150			155					
CAG	TGG	TGT	GAT	CAC	AGC	TCA	CTG	CAG	CCT	TCA	ACT	CCT	GAG	ATC	AAG		530
Gln	Trp	Cys	Asp	His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys		
							160		165			170					
CAT	CCT	CCT	GCC	TCA	GCC	TCC	CAA	GTA	GCT	GGG	ACC	AAA	GAC	ATG	CAC		578
His	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His		
							175		180			185					
CAC	TAC	ACC	TGG	CTA	ATT	TTT	ATT	TTT	ATT	TTT	AAT	TTT	TTG	AGA	CAG		626
His	Tyr	Thr	Trp	Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln		
							190		195			200					
AGT	CTC	AAC	TCT	GTC	ACC	CAG	GCT	GGA	GTG	CAG	TGG	CGC	AAT	CTT	GGC		674
Ser	Leu	Asn	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly		
							205		210			215		220			
TCA	CTG	CAA	CCT	CTG	CCC	GGG	TTC	AAG	TTA	TTC	TCC	TGC	CCC	AGC		722	
Ser	Leu	Gln	Pro	Leu	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser			
							225		230			235					
CTC	CTG	AGT	AGC	TGG	GAC	TAC	AGG	CGC	CCA	CCA	CGC	CTA	GCT	AAT	TTT		770
Leu	Leu	Ser	Ser	Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe		
							240		245			250					
TTT	GTA	TTT	TTA	GTA	GAG	ATG	GGG	TTC	ACC	ATG	TTC	GCC	AGG	TTG	ATC		818
Phe	Val	Phe	Leu	Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile		
							255		260			265					
TTG	ATC	TCT	GGA	CCT	TGT	GAT	CTG	CCT	GCC	TCG	GCC	TCC	CAA	AGT	GCT		866

85	90	95
Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp		
100	105	110
Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp		
115	120	125
Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu		
130	135	140
Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp		
145	150	160
His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala		
165	170	175
Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp		
180	185	190
Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser		
195	200	205
Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro		
210	215	220
Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser		
225	230	240
Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu		
245	250	255
Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly		
260	265	270
Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly		
275	280	285
Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met		
290	295	300
Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly		
305	310	320
Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser		
325	330	335
Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn		
340	345	350
Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp		
355	360	365
Ser Gln Thr Pro Asp Leu Arg		
370	375	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTGCCAGG CTGGAGTGCA ATGGCGCAAT 60
CTCAGCTCAC CGAACCTCC GCCTCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGATTT TTTTTAGTA 180
GAGATGGAGT TAACTCCAT GTGGTCAGG CTGGTCTCGA ACTCCGACC TCAGATGATC 240
TCCCGTCTCG GCCTGCCAA AGTGTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC 300
TGCCTGGCTA ATTTTGTTG TAGAACAGG GTTCACTGA TGTTGCCAA GCTGGTCTCC 360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCGTCAGCC 420
GTGCCTGGCC TTTTATTTT ATTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT 480
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTCAA CTCCTGAGAT CAAGCAATCC 540
TCCTGCCTCA GCCTCCCAAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600
TTTATTTTA TTTTAATT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660
AGTGGCGAA TCTTGGCTCA CTGCAACCTC TGCTCCGG GTTCAAGTTA TTCTCCTGCC 720
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTGTAT 780
TTTTAGTAGA GATGGGGTTT CACCATGTTG GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGCGTGACT CCACGCCGGC 900
CTATTTTAA TTTTGTTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
AATGGCAAAT CTCGGCTACT CGAACCTCT GCCTCCGGG TCAAGCGATT CTCCTGTCTC 1020
AGCCTCCAA GCAGCTGGGA TTACGGGACC TGCACCAACAC CCCGCTAATT TTTGTATTT 1080
CATTAGAGGC GGGTTTACCA TATTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140
CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
GGCTAATTG GAATAAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGGCCAC AACACCCAGC CAGTCACATT 1320
TTTTAACAG TTACATCTT ATTGAGTAT ACTAGAAAGT AATACAATAA ACATGTAAA 1380
C 1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTGCCAGG CTGGAGTGCA ATGGCGCAAT 60
CTCAGCTCAC CGAACCTCC GCCTCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT 180
AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT 240
CCCGTCTCGG CCTCCCAAAG TGCTAGATAc AGGACTGAGC ACCATGCCCG GCCTCTGCCT 300
GGCTAATTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT 360
CAAGCAGTCC ACCTGCCTCA GCCTCCAAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC 420
TGGCCTTTT ATTTTATTT TTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480
GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540
TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTAT 600
TTTTATTTT AATTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660
GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCAGGTTTC AAGTTATTCT CCTGCCAG 720
CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCA GCTAATTTT TTGTATTTT 780
AGTAGAGATG GGGTTTCACC ATGTTGCCA GGTTGATGCT AGATCTCTG ACCTTGTGAT 840
CTGCCTGCCT CGGCCTCCC AAGTGCTGGG ATTACAGGAC GTGACGCCA CCGCCCGGCC 900
TATTTTAAT TTTGTTTGT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA 960
ATGGCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCGGG CTCAAGCGAT TCTCCTGTCT 1020
CAGCCTCCC AGCAGCTGGG ATTACGGCA CCTGCACCAC ACCCCGCTAA TTTTGTATT 1080
TTCATTAGAG GCGGGGTTTC ACCATATTG TCAGGCTGGT CTCAAACCTCC TGACCTCAGG 1140
TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGCAGACGC CTCACCCAGC 1200
CGGCTAATT AGATAAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG 1260
GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC 1320
ATTTTAAAC AGTTACATCT TTATTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG 1380
AACCTGCAAAT TTGAGTAGT ACAGAGTCTT TTATAACT 1418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14